

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

### (i) APPLICANT:

5 (A) NAME: Vlaams Interuniversitair Instituut voor  
Biotechnologie  
(B) STREET: Rijvisschestraat 120  
(C) CITY: Zwijnaarde  
(E) COUNTRY: Belgium  
(F) POSTAL CODE (ZIP): 9052B  
10 (G) TELEPHONE: +32 9 2446611  
(H) TELEFAX: +32 9 2446610

(ii) TITLE OF INVENTION: CD40 interacting and TRAF interacting proteins

15 (iii) NUMBER OF SEQUENCES: 6

### (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

### (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1920 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

### (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

### (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 20..1108

### 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTGCAGAGGC GGCAGGAAGA TGGAGTTGGG GAGTTGCCTG GAGGGCGGGA GGGAGGCGGC	60
GGAGGAAGAG GGCGAGCCTG AGGTGAAAAA GCGGCGACTT CTGTGTGTGG AGTTTGCCTC	120
GGTCGCAAGC TGCGATGCCG CAGTGGCTCA GTGCTTCCTG GCCGAGAACG ACTGGGAGAT	180
GGAAAGGGCT CTGAACTCCT ACTTCGAGCC TCCGGTGGAG GAGAGCGCCT TGAACGCCG	240
40 ACCTGAAACC ATCTCTGAGC CCAAGACCTA TGTTGACCTA ACCAATGAAG AAACAAGTGA	300
TTCCACCACT TCTAAATCA GCCCATCTGA AGATACTCAG CAAGAAAATG GCAGCATGTT	360
CTCTCTCATT ACCTGGAATA TTGATGGATT AGATCTAAAC AATCTGTCAG AGAGGGCTCG	420

	AGGGGTGTGT TCCCTAG CTTTGTACAG CCCAGATGTG ATATTTCTT GGAAGTTAT	480
	TCCCCCATAT TATAGCTACC TAAAGAAGAG ATCAAGTAAT TATGAGATTA TTACAGGTCA	540
	TGAAGAAGGA TATTTACAG CTATAATGTT GAAGAAATCA AGAGTGAAAT TAAAAAGCCA	600
	AGAGATTATT CCTTTTCCAA GTACCAAAAT GATGAGAAAC CTTTATGTG TGCATGTGAA	660
5	TGTGTCAGGA AATGAGCTTT GCCTTATGAC ATCCCATTG GAGAGCACCA GAGGGCATGC	720
	TGCGGAACGA ATGAATCAGT TAAAAATGGT TTAAAGAAA ATGCAAGAGG CTCCAGAGTC	780
	AGCTACAGTT ATATTTGCAG GAGATACAAA TCTAAGGGAT CGAGAGGTTA CCAGATGTGG	840
	TGGTTTACCC AACAACATTG TGGATGTCTG GGAGTTTTTG GGCAAACCTA AACATTGCCA	900
	GTATACATGG GATACACAAA TGAAGCTCTAA TCTTGAATA ACTGCTGCTT GTAACTTCG	960
10	TTTTGATCGA ATATTTTCA GAGCAGCAGC AGAAGAGGGA CACATTATTC CCCGAAGTTT	1020
	GGACCTTCTT GGATTAGAAA AACTGGACTG TGGTAGATTT CCTAGTGATC ACTGGGGTCT	1080
	TCTGTGCAAC TTAGATATAA TATTGTAAAA TGCTTTTCAA GTGTGGGTTT TGCCCTGATT	1140
	GTTGCAAATA CAATTTCCAC CTTCTGGAAA GGTAGGTTTG CTGTGGAGGA AATAATGTAC	1200
	TAGATCATTG TCACAGAAAA ACCAACTATG ATTTATGGTT GTGTTTTAG AATTCAACAT	1260
15	TAAAGATTAA TGTTTATTTA AACGAACACA TTCCTGCATT CAGGATGTGA GGCCATTTAA	1320
	TAAAAAGGGC ACAAAGCCTG TCAGAGTTTT CAACGGTGCT TACAGCTGCC AGCTGGATTC	1380
	CAAACAGGTA CCCCATGTG TCTGAGCTAA TGTTTATATT TTTCCATTCA GGCACCGAAA	1440
	TAGTTAATAT TTTAAATAAG TCTTCAAAAG AAAACATAAG AGATTATTGA GTTCTTGGGA	1500
	CTGGATCCTT TATTTCATAA GTTCAGATCA TCTTAAATGA AAATGCCATG ATTATCTGCA	1560
20	GTTAAGTAGA TGACAGCTAT TCTACATCAG ACTTGATTTT TGTCAGCTAA TTACATAATT	1620
	GGTAAGNTAT AATTGAAACC TTATGGCTTA AAATTCCTTA ACTCCTTTTT GATTCATGTT	1680
	TGTAGTCATG TTGTCAACAG AGGCAAAGTT AAGCTTGATG ATGGTTAAAA TCGGTTTGAT	1740
	AGCACCATGG GACATTTTTT TAACAAAAAT AAATGCATGA AGAGACATAG CCTTTTAGTT	1800
	TTGCTAATTG TGAAATGGAA ATGCTTTACA GGAAGTAAAT GCAAATTANT TTTAAGTGTG	1860
25	CTTTAAAGAA AAATATTTTC CCCACAGGAG AAATTTAAAT AAAGAATTTT ATTTGGTAAA	1920

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

5 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu  
1 5 10 15  
Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe  
20 25 30  
Ala Ser Val Ala Ser Cys Asp Ala Val Ala Gln Cys Phe Leu Ala  
35 40 45  
10 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro  
50 55 60  
Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu  
65 70 75 80  
15 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr  
85 90 95  
Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser  
100 105 110  
Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn  
115 120 125  
20 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser  
130 135 140  
Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr  
145 150 155 160  
25 Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu  
165 170 175  
Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys  
180 185 190  
Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu  
195 200 205  
30 Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr  
210 215 220  
Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln  
225 230 235 240  
35 Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr  
245 250 255  
Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg  
260 265 270  
Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly  
275 280 285  
40 Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn  
290 295 300  
Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe



					0					105					110				
		AGT Ser	CCA Pro	TCT Ser	GGA Gly	ACT Thr	CCT Pro	CTA Leu	GAA Glu	GAT Asp	AGC Ser	AGC Ser	ACT Thr	ATT Ile	TCT Ser	TTC Phe	ATT Ile		502
					115					120					125				
5		ACC Thr	TGG Trp	AAT Asn	ATT Ile	GAT Asp	GGA Gly	TTA Leu	GAT Asp	GGA Gly	TGC Cys	AAT Asn	CTG Leu	CCC Pro	GAG Glu	AGG Arg	GCT Ala		550
				130					135					140					
		CGA Arg	GGG Gly	GTG Val	TGT Cys	TCC Ser	TGC Cys	CTA Leu	GCT Ala	TTG Leu	TAT Tyr	AGT Ser	CCA Pro	GAT Asp	GTG Val	GTA Val	TTT Phe		598
10			145					150					155						
		CTA Leu	CAG Gln	GAA Glu	GTT Val	ATC Ile	CCC Pro	CCA Pro	TAC Tyr	TGT Cys	GCC Ala	TAC Tyr	CTA Leu	AAG Lys	AAG Lys	AGA Arg	GCA Ala		646
							165					170					175		
15		GCC Ala	AGT Ser	TAC Tyr	ACA Thr	ATT Ile	ATT Ile	ACA Thr	GGT Gly	AAT Asn	GAA Glu	GAA Glu	GGA Gly	TAT Tyr	TTC Phe	ACA Thr	GCT Ala		694
						180					185					190			
		ATA Ile	CTA Leu	TTG Leu	AAG Lys	AAA Lys	GGA Gly	AGA Arg	GTG Val	AAA Lys	TTT Phe	AAA Lys	AGT Ser	CAG Gln	GAG Glu	ATT Ile	ATT Ile		742
					195					200				205					
20		CCT Pro	TTT Phe	CCA Pro	AAT Asn	ACC Thr	AAA Lys	ATG Met	ATG Met	AGA Arg	AAC Asn	CTG Leu	CTA Leu	TGC Cys	GTA Val	AAT Asn	GTG Val		790
				210					215					220					
		AGT Ser	TTG Leu	GGT Gly	GGA Gly	AAT Asn	GAA Glu	TTT Phe	TGC Cys	CTT Leu	ATG Met	ACA Thr	TCC Ser	CAT His	TTG Leu	GAG Glu	AGC Ser		838
25			225					230					235						
		ACC Thr	AGA Arg	GAA Glu	CAT His	TCT Ser	GCG Ala	GAA Glu	CGA Arg	ATA Ile	AGA Arg	CAA Gln	TTA Leu	AAA Lys	ACT Thr	GTT Val	CTT Leu		886
							245					250					255		
		GGA Gly	AAA Lys	ATG Met	CAA Gln	GAG Glu	GCT Ala	CCA Pro	GAT Asp	TCA Ser	ACC Thr	ACG Thr	GTT Val	ATA Ile	TTT Phe	GCA Ala	GGA Gly		934
30					260						265					270			
		GAT Asp	ACA Thr	AAT Asn	TTA Leu	AGA Arg	GAT Asp	CAA Gln	GAA Glu	GTT Val	ATC Ile	AAA Lys	TGT Cys	GGT Gly	GGT Gly	TTA Leu	CCT Pro		982
					275					280				285					
35		GAC Asp	AAC Asn	GTT Val	TTT Phe	GAT Asp	GCC Ala	TGG Trp	GAA Glu	TTT Phe	TTA Leu	GGC Gly	AAA Lys	CCT Pro	AAA Lys	CAT His	TGC Cys		1030
				290					295					300					
		CAG Gln	TAT Tyr	ACA Thr	TGG Trp	GAT Asp	ACG Thr	AAA Lys	GCA Ala	AAT Asn	AAC Asn	AAC Asn	CTC Leu	AGG Arg	ATC Ile	CCT Pro	GCT Ala		1078
40			305					310					315						
		GCT Ala	TAT Tyr	AAG Lys	CAT His	CGT Arg	TTT Phe	GAT Asp	CGA Arg	ATA Ile	TTT Phe	TTC Phe	AGA Arg	GCA Ala	GAA Glu	GAG Glu	GGG Gly		1126
						325					330						335		
		CAC His	CTT Leu	ATT Ile	CCT Pro	CAA Gln	AGT Ser	TTA Leu	GAC Asp	CTT Leu	GTT Val	GGG Gly	TTG Leu	GAA Glu	AAA Lys	CTG Leu	GAC Asp		1174
45					340					345						350			
		TGT Cys	GGT Gly	AGA Arg	TTT Phe	CCG Pro	AGT Ser	GAT Asp	CAC His	TGG Trp	GGG Gly	CTC Leu	TTG Leu	TGC Cys	ACC Thr	TTG Leu	AAT Asn		1222
					355					360					365				

GTA GTA TTG TG AGCTTCCC ACTTGCAGCT TTACACGTTT GTT CTA  
 Val Val Leu \*  
 370

1274

GTTCTGAATT TGTGTAGGTC TCAACCTTTC AGGACATC

1312

5 (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 371 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Ala	Ser	Gly	Ser	Ser	Ser	Asp	Ala	Ala	Glu	Pro	Ala	Gly	Pro	Ala	1	5	10	15
Gly	Arg	Ala	Ala	Ser	Ala	Pro	Glu	Ala	Ala	Gln	Ala	Glu	Glu	Asp	Arg	20	25	30	
Val	Lys	Arg	Arg	Arg	Leu	Gln	Cys	Leu	Gly	Phe	Ala	Leu	Val	Gly	Gly	35	40	45	
Cys	Asp	Pro	Thr	Met	Val	Pro	Ser	Val	Leu	Arg	Glu	Asn	Asp	Trp	Gln	50	55	60	
Thr	Gln	Lys	Ala	Leu	Ser	Ala	Tyr	Phe	Glu	Leu	Pro	Glu	Asn	Asp	Gln	65	70	75	80
Gly	Trp	Pro	Arg	Gln	Pro	Pro	Thr	Ser	Phe	Lys	Ser	Glu	Ala	Tyr	Val	85	90	95	
Asp	Leu	Thr	Asn	Glu	Asp	Ala	Asn	Asp	Thr	Thr	Ile	Leu	Glu	Ala	Ser	100	105	110	
Pro	Ser	Gly	Thr	Pro	Leu	Glu	Asp	Ser	Ser	Thr	Ile	Ser	Phe	Ile	Thr	115	120	125	
Trp	Asn	Ile	Asp	Gly	Leu	Asp	Gly	Cys	Asn	Leu	Pro	Glu	Arg	Ala	Arg	130	135	140	
Gly	Val	Cys	Ser	Cys	Leu	Ala	Leu	Tyr	Ser	Pro	Asp	Val	Val	Phe	Leu	145	150	155	160
Gln	Glu	Val	Ile	Pro	Pro	Tyr	Cys	Ala	Tyr	Leu	Lys	Lys	Arg	Ala	Ala	165	170	175	
Ser	Tyr	Thr	Ile	Ile	Thr	Gly	Asn	Glu	Gly	Tyr	Phe	Thr	Ala	Ile		180	185	190	
Leu	Leu	Lys	Lys	Gly	Arg	Val	Lys	Phe	Lys	Ser	Gln	Glu	Ile	Ile	Pro	195	200	205	
Phe	Pro	Asn	Thr	Lys	Met	Met	Arg	Asn	Leu	Leu	Cys	Val	Asn	Val	Ser	210	215	220	
Leu	Gly	Gly	Asn	Glu	Phe	Cys	Leu	Met	Thr	Ser	His	Leu	Glu	Ser	Thr	225	230	235	240
Arg	Glu	His	Ser	Ala	Glu	Arg	Ile	Arg	Gln	Leu	Lys	Thr	Val	Leu	Gly	245	250	255	

Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Gly Asp  
 265 265 270  
 Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp  
 275 280 285  
 5 Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln  
 290 295 300  
 Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala  
 305 310 315 320  
 10 Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His  
 325 330 335  
 Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys  
 340 345 350  
 Gly Arg Phe Pro Ser Asp His Trp Gly Leu Leu Cys Thr Leu Asn Val  
 355 360 365  
 15 Val Leu \*  
 370

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1536 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 209..1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGAGAAAGAG GCTCCGGGGA GATAGCGGAC CAGTGAGGGC TGCCCCCTCTT TTGAAGCGGT 60  
 TTTCGTCTCT TTCCGCCAGT GGCCTCCCAG CTCACGCAGG GCGGGGTCCC GGTAGCGCGA 120  
 GCGGTGTCAG GCGGGAAGG GGAGTGGTGG CGGCTGCGGC AGTAGGGACA GCAGGAGCAG 180  
 35 TGGTGCTGTC AGCGCGGCCG TCGGAGACAT GGGAGACCCG GGGTCGGAAA TAATAGAATC 240  
 TGTCCCTCCA GCTGGCCCTG AGGCATCTGA GTCAACAACG GATGAAAATG AAGACGACAT 300  
 TCAGTTTGTC AGTGAAGGAC CATCGAGACC TGTTCTTGAA TACATCGATC TGGTCTGTGG 360  
 TGATGATGAA AACCCTAGCG CCTATTATAG TGATATTCTG TTTCCTAAAA TGCCAAAACG 420  
 ACAGGGTGAT TTTTTCATT TTTTAAATAT GAAGAAGGTG AAAACAGACA CAGAAAATAA 480  
 40 TGAAGTGAGC AAAAATCACT GCAGATTGTC TAAGGCAAAG GAACCACATT TCGAGTATAT 540

AGAACAACCA ATC AAG AAAAGCCATC ACTTTCATCA AAGAAAGA TAGATAATCT 600  
TGTGCTTCCA GATTGTTGGA ATGAAAAACA AGCATTATG TTTACAGAAC AATACAAATG 660  
GCTTGAAATA AAAGAAGGTA AATTAGGATG TAAGGATTGT TCAGCAGTTC GGCATTTGGG 720  
ATCGAAAGCA GAAAAGCATG TCCATGTGTC CAAGGAATGG ATTGCATATT TAGTAACCCC 780  
5 TAATGGCAGT AATAAACTA CTAGCAAGC TTCTCTACGA AAAAAATTA GGGAACATGA 840  
TGTTTCTAAA GCCCATGGTA AAATTCAGGA TTTGTTAAAG GAATCAACTA ATGATTCAAT 900  
TTGTAATTTA GTGCATAAAC AAAATAATAA AAATATTGAT GCTACTGTAA AAGTTTTCAA 960  
TACTGTTTAC AGTTTAGTAA AACATAACAG ACCTTTATCT GATATTGAGG GGGCAAGAGA 1020  
ATTACAGGAA AAAAATGGAG AGGTAAATTG TTAAATACA CGTTACAGTG CAACAAGAAT 1080  
10 AGCAGAACAT ATTGCAAAAG AAATGAAGAT GAAGATATTT AAGAATATTA TAGAAGAGAA 1140  
TGCCAAAATC TGTATCATAA TTGATGAGGC ATCTACAGTT TCAAAGAAAA CCACCCTAGT 1200  
GATTTATCTC CAGTGCACAA TTCAGTCAGC TCCTGCACCT GTTATGTTAT TTGTGGCTTT 1260  
AAAAGAATTG GTGTCAACTA TAGCAGAGTG TATTGTCAAT ACATTATTGA CTACTTTTAA 1320  
TGATTGTGGT TTTACAAATG AATATTTGAA AGCAAATTTA ATTGCATTTT GTTCTGATGG 1380  
15 TGCTAATACA ANCCTGGGAA GAAAGTCTGG AGTAGCTACA AAATTGTTAG AAAATTTTCC 1440  
TGAAATCATC ATTTGGAAC TTTTAAATCA TCGATTACAA TTGTCACTTG ATGATTCTAT 1500  
ATCCGAAATA AAACAAATTA ATCATTTAAN NTATAA 1536

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 442 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

30 Met Gly Asp Pro Gly Ser Glu Ile Ile Glu Ser Val Pro Pro Ala Gly  
1 5 10 15  
Pro Glu Ala Ser Glu Ser Thr Thr Asp Glu Asn Glu Asp Asp Ile Gln  
20 25 30  
35 Phe Val Ser Glu Gly Pro Ser Arg Pro Val Leu Glu Tyr Ile Asp Leu  
35 40 45  
Val Cys Gly Asp Asp Glu Asn Pro Ser Ala Tyr Tyr Ser Asp Ile Leu



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	50	55	6
	Phe 65	Pro Lys Met Pro Lys Arg Gln Gly Asp 70	Phe Leu His Phe Leu Asn 75 80
5	Met Lys Lys Val 85	Lys Thr Asp Thr Glu Asn Asn Glu Val Ser Lys Asn 90 95	
	His Cys Arg 100	Leu Ser Lys Ala Lys Glu Pro His Phe Glu Tyr Ile Glu 105 110	
	Gln Pro Ile Ile 115	Glu Glu Lys Pro Ser Leu Ser Ser Lys Lys Glu Ile 120 125	
10	Asp Asn Leu Val Leu Pro 130	Asp Cys Trp Asn Glu Lys Gln Ala Phe Met 135 140	
	Phe Thr Glu Gln Tyr 145	Lys Trp Leu Glu Ile Lys Glu Gly Lys Leu Gly 150 155 160	
15	Cys Lys Asp Cys 165	Ser Ala Val Arg His Leu Gly Ser Lys Ala Glu Lys 170 175	
	His Val His Val 180	Ser Lys Glu Trp Ile Ala Tyr Leu Val Thr Pro Asn 185 190	
	Gly Ser Asn Lys Thr Thr 195	Arg Gln Ala Ser Leu Arg Lys Lys Ile Arg 200 205	
20	Glu His Asp Val Ser Lys 210	Ala His Gly Lys Ile Gln Asp Leu Leu Lys 215 220	
	Glu Ser Thr Asn Asp 225	Ser Ile Cys Asn Leu Val His Lys Gln Asn Asn 230 235 240	
25	Lys Asn Ile Asp 245	Ala Thr Val Lys Val Phe Asn Thr Val Tyr Ser Leu 250 255	
	Val Lys His Asn Arg Pro Leu Ser 260	Asp Ile Glu Gly Ala Arg Glu Leu 265 270	
	Gln Glu Lys Asn Gly Glu Val 275	Asn Cys Leu Asn Thr Arg Tyr Ser Ala 280 285	
30	Thr Arg Ile Ala Glu His 290	Ile Ala Lys Glu Met Lys Met Lys Ile Phe 295 300	
	Lys Asn Ile Ile Glu Glu Asn Ala Lys 305	Ile Cys Ile Ile Ile Asp Glu 310 315 320	
35	Ala Ser Thr Val 325	Ser Lys Lys Thr Thr Leu Val Ile Tyr Leu Gln Cys 330 335	
	Thr Ile Gln Ser Ala Pro Ala Pro 340	Val Met Leu Phe Val Ala Leu Lys 345 350	
	Glu Leu Val Ser Thr Ile Ala Glu Cys 355	Ile Val Asn Thr Leu Leu Thr 360 365	
40	Thr Leu Asn Asp Cys Gly Phe Thr 370	Asn Glu Tyr Leu Lys Ala Asn Leu 375 380	
	Ile Ala Phe Cys Ser 385	Asp Gly Ala Asn Thr Xaa Leu Gly Arg Lys Ser 390 395 400	

Gly Val A [redacted] hr Lys Leu Leu Glu Asn Phe Pro Glu [redacted] a Ile Ile Trp  
405 410 415

Asn Cys Leu Asn His Arg Leu Gln Leu Ser Leu Asp Asp Ser Ile Ser  
420 425 430

5 Glu Ile Lys Gln Ile Asn His Leu Xaa Tyr  
435 440

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